

In the Claims

1. (Reiterated) An isolated nucleic acid sequence encoding a prenyltransferase.
2. (Reiterated) An isolated nucleic acid sequence according to Claim 1, wherein said prenyltransferase is selected from the group consisting of straight chain prenyltransferase and aromatic prenyltransferase.
3. (Reiterated) An isolated DNA sequence according to Claim 1, wherein said nucleic acid sequence is isolated from a eukaryotic cell source.
4. (Reiterated) An isolated DNA sequence according to Claim 3, wherein said eukaryotic cell source is selected from the group consisting of mammalian, nematode, fungal, and plant cells.
5. (Reiterated) The DNA encoding sequence of Claim 4 wherein said prenyltransferase protein is from *Arabidopsis*.
6. (Amended) The DNA encoding sequence of Claim 5 wherein said prenyltransferase protein is encoded by a sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 12 and 17.
7. (Reiterated) The DNA encoding sequence of Claim 4 wherein said prenyltransferase protein is from corn.
8. (Reiterated) The DNA encoding sequence of Claim 7 wherein said prenyltransferase protein is encoded by a sequence which includes the EST of the sequences of Figure 3.
9. (Reiterated) The DNA encoding sequence of Claim 4 wherein said prenyltransferase protein is from soybean.
10. (Reiterated) The DNA encoding sequence of Claim 9 wherein said prenyltransferase protein is encoded by a sequence which includes the ESTs of the group consisting of the sequences of Figure 2 and Figure 9.
11. (Reiterated) An isolated DNA sequence according to Claim 1, wherein said nucleic

acid sequence is isolated from a prokaryotic cell source.

12. (Reiterated) An isolated DNA sequence according to Claim 11, wherein said prokaryotic source is *Synechocystis*.

13. (Reiterated) A nucleic acid construct comprising as operably linked components, a transcriptional initiation region functional in a host cell, a nucleic acid sequence encoding prenyltransferase, and a transcriptional termination region.

14. (Reiterated) A nucleic acid construct according to Claim 13, wherein said nucleic acid sequence encoding prenyltransferase is obtained from an organism selected from the group consisting of a eukaryotic organism and a prokaryotic organism.

15. (Reiterated) A nucleic acid construct according to Claim 14, wherein said nucleic acid sequence encoding prenyltransferase is obtained from a plant source.

16. (Reiterated) A nucleic acid construct according to Claim 15, wherein said nucleic acid sequence encoding prenyltransferase is obtained from a source selected from the group consisting of *Arabidopsis*, soybean and corn.

17. (Reiterated) A nucleic acid construct according to Claim 13, wherein said nucleic acid sequence encoding prenyltransferase is obtained from *Synechocystis*.

18. (Reiterated) A plant cell comprising the construct of Claim 13.

19. (Amended) A method for the alteration of the tocopherol content in a host cell, comprising transforming said host cell with a construct comprising as operably linked components, a transcriptional initiation region functional in a host cell, a nucleic acid sequence encoding prenyltransferase, and a transcriptional termination region.

20. (Reiterated) The method according to Claim 19, wherein said host cell is selected from the group consisting of a prokaryotic cell and a eukaryotic cell.

21. (Reiterated) The method according to Claim 20, wherein said prokaryotic cell is *Synechocystis*.

22. (Reiterated) The method according to Claim 20, wherein said eukaryotic cell is a

plant cell.

23. (Reiterated) The method according to Claim 22, wherein said plant cell is obtained from a plant selected from the group consisting of *Arabidopsis*, soybean, and corn.

24. (Reiterated) A method for producing a tocopherol compound of interest in a host cell, said method comprising obtaining a transformed host cell, said host cell having and expressing in its genome:

a construct having a DNA sequence encoding a prenyltransferase operably linked to a transcriptional initiation region functional in a host cell,

wherein said prenyltransferase is involved in the synthesis of tocopherols.

25. (Reiterated) The method according to Claim 24, wherein said host cell is selected from the group consisting of a prokaryotic cell and a eukaryotic cell.

26. (Reiterated) The method according to Claim 25, wherein said prokaryotic cell is *Synechocystis*.

27. (Reiterated) The method according to Claim 24, wherein said eukaryotic cell is a plant cell.

28. (Reiterated) The method according to Claim 27, wherein said plant cell is obtained from a plant selected from the group consisting of *Arabidopsis*, soybean, and corn.

29. (Reiterated) A method for increasing the biosynthetic flux in cell from a host cell toward tocopherol production, said method comprising transforming said host cell with a construct comprising as operably linked components, a transcriptional initiation region functional in a host cell, a DNA encoding a prenyltransferase involved in the synthesis of tocopherols and a transcriptional termination region.

30. (Reiterated) The method according to Claim 29, wherein said host cell is selected from the group consisting of a prokaryotic cell and a eukaryotic cell.

31. (Reiterated) The method according to Claim 30, wherein said prokaryotic cell is *Synechocystis*.